Appendix A: Marked Up Copy of Amended Claims

66. An isolated nucleic acid for use as a probe or primer which comprises a sequence that encodes an amino acid sequence that is partly, substantially, or completely conserved between a VRN2 sequence of SEQ ID Nos. 2, 5, or 8, and at least one of the other sequences shown in Figure 8a (SEQ ID Nos. 2, 12, 10, 14, and 16) or 8b (SEQ ID Nos. 17-38), wherein said nucleic acid is 15 to 40 nucleotides in length.

70. A pair of primers according to claim 69 which is selected from:

VRN2-AP (SEQ ID NO:67) and VRN2-AJ (SEQ ID NO:63);
VRN2-AO (SEQ ID NO:66) and VRN2-AS (SEQ ID NO:70); and
VRN2-AI (SEQ ID NO:62) and VRN2-AJ (SEQ ID NO:63).

73. A method for identifying or cloning a nucleic acid selected from the group consisting of SEQ ID NO: 1, SEQ ID: NO: 3, SEQ ID NO: 4, SEQ ID NO: 6, and SEQ ID NO: 7, which method employs a probe or primer, said probe or primer comprising a sequence that encodes an amino acid sequence that is partly, substantially or completely conserved between a VRN2 sequence of SEQ ID Nos. 2, 5 or 8 and at least one of the other sequences shown in Figure 8a (SEQ ID Nos. 2, 12, 10, 14, and 16) or 8b (SEQ ID Nos. 17-38), wherein said nucleic acid is 15 to 40 nucleotides in length or a pair of primers selected from the group consisting of VRN2-AP (SEQ ID NO:67) and VRN2-AJ (SEQ ID NO:63); VRN2-AO (SEQ ID NO:66) and VRN2-AS (SEQ ID NO:70); and VRN2-AI (SEQ ID NO:62) and VRN2-AJ (SEQ ID NO:63).

74. A method for determining the presence of a nucleic acid according claim 60 within the genetic make-up of a plant, which method employs a probe or primer, said probe or primer

comprising a sequence that encodes an amino acid sequence that is partly, substantially or completely conserved between a VRN2 sequence of SEQ ID Nos. 2, 5 or 8 and at least one of the other sequences shown in Figure 8a (SEQ ID Nos. 2, 12, 10, 14, and 16) or 8b (SEQ ID Nos. 17-38), wherein said nucleic acid is 15 to 40 nucleotides in length, or a pair of primers selected from the group consisting of VRN2-AP (SEQ ID NO:67) and VRN2-AJ (SEQ ID NO:63); VRN2-AO (SEQ ID NO:66) and VRN2-AS (SEQ ID NO:70); and VRN2-AI (SEQ ID NO:62) and VRN2-AJ (SEQ ID NO:63).

75. A method according to claim 73, which comprises the steps of:

(a) providing a preparation of nucleic acid from a plant cell;

(b) providing a nucleic acid molecule which is a probe, said probe comprising a sequence that encodes an amino acid sequence that is partly, substantially or completely conserved between a VRN2 sequence of SEQ ID Nos. 2, 5 or 8 and at least one of the other sequences shown in Figure 8a (SEQ ID Nos. 2, 12, 10, 14, and 16) or 8b (SEQ ID Nos. 17-38), wherein said probe is 15 to 40 nucleotides in length;

(c) contacting nucleic acid in said preparation with said probe under conditions for hybridisation; and

(d) identifying a nucleic acid selected from the group consisting of SEQ ID NO: 1, SEQ ID: NO: 3, SEQ ID NO: 4, SEQ ID NO: 6, and SEQ ID NO: 7, if present by its hybridisation with said nucleic acid probe.

76. A method according to claim 73, which method comprises the steps of:

(a) providing a preparation of nucleic acid from a plant cell;

(b) providing a pair of nucleic acid molecule primers suitable for PCR, at least one of said primers being a primer which comprises a sequence that encodes an amino acid sequence that is partly, substantially or completely conserved between a VRN2 sequence of SEQ ID Nos. 2, 5 or 8 and at least one of the other sequences shown in Figure 8a (SEQ ID Nos. 2, 12, 10, 14, and 16) or 8b (SEQ ID Nos. 17-38), wherein said nucleic acid is 15 to 40 nucleotides in length;

(c) contacting nucleic acid in said preparation with said primers under conditions for performance of PCR;

(d) performing PCR and determining the presence or absence of an amplified PCR product.

77. A method according to claim 76 wherein the pair of nucleic acid molecule primers are
VRN2-AP (SEQ ID NO:67) and VRN2-AJ (SEQ ID NO:63);
VRN2-AO (SEQ ID NO:66) and VRN2-AS (SEQ ID NO:70); and
VRN2-AI (SEQ ID NO:62) and VRN2-AJ (SEQ ID NO:63).

78. A method of selecting a plant having a desired allele of the VRN2 gene, which method employs a probe or primer, said probe or primer comprising a sequence that encodes an amino acid sequence that is partly, substantially or completely conserved between a VRN2 sequence of SEQ ID Nos. 2, 5 or 8 and at least one of the other sequences shown in Figure 8a (SEQ ID Nos. 2, 12, 10, 14, and 16) or 8b (SEQ ID Nos. 17-38), wherein said nucleic acid is 15 to 40 nucleotides in length, or a pair of primers selected from the group consisting of
VRN2-AP (SEQ ID NO:67) and VRN2-AJ (SEQ ID NO:63);
VRN2-AO (SEQ ID NO:66) and VRN2-AS (SEQ ID NO:70); and
VRN2-AI (SEQ ID NO:62) and VRN2-AJ (SEQ ID NO:63).

Appendix B - Annex B of the PCT Applicant's Guide

(c) **Independent and Dependent Claims.** Unity of invention has to be considered in the first place only in relation to the independent claims in an international application and not the dependent claims. By "dependent" claim is meant a claim which contains all the features of another claim and is in the same category of claim as that other claim (the expression "category of claim" referring to the classification of claims according to the subject matter of the invention claimed–for example, product, process, use or apparatus or means, etc.).(I) If the independent claims avoid the prior art and satisfy the requirement of unity of invention, no problem of lack of unity arises in respect of any claims that depend on the independent claims. In particular, it does not matter if a dependent claim itself contains a further invention.

Equally, no problem arises in the case of a genus/species situation where the genus claim avoids the prior art. Moreover, no problem arises in the case of a combination/subcombination situation where the subcombination claim avoids the prior art and the combination claim includes all the features of the subcombination.

(e) **Combinations of Different Categories of Claims.** The method for determining unity of invention under Rule 13 shall be construed as permitting, in particular, the inclusion of any one of the following combinations of claims of different categories in the same international application:

(I) in addition to an independent claim for a given product, an independent claim for a process specially adapted for the manufacture of the said product, and an independent claim for a use of the said product, or...

Appendix C - Copy of Pages from Preliminary Amendment

The required pages 6, 8, and 10 of the preliminary amendment filed November 21, 2001 are attached hereto.

which comprises a sequence that encodes an amino acid sequence that is partly, substantially or completely conserved between a VRN2 sequence of SEQ ID Nos. 2, 5 or 8 and at least one of the other sequences shown in Figure 8a or 8b, wherein said nucleic acid is 15 to 40 nucleotides in length;

(c) contacting nucleic acid in said preparation with said primers under conditions for performance of PCR;

(d) performing PCR and determining the presence or absence of an amplified PCR product.

77. A method according to claim 76 wherein the pair of nucleic acid molecule primers are VRN2-AP and VRN2-AJ;
VRN2-AO and VRN2-AS; and
VRN2-AI and VRN2-AJ.

78. A method of selecting a plant having a desired allele of the VRN2 gene, which method employs a probe or primer, said probe or primer comprising a sequence that encodes an amino acid sequence that is partly, substantially or completely conserved between a VRN2 sequence of SEQ ID Nos. 2, 5 or 8 and at least one of the other sequences shown in Figure 8a or 8b, wherein said nucleic acid is 15 to 40 nucleotides in length, or a pair of primers selected from the group consisting of
VRN2-AP and VRN2-AJ;
VRN2-AO and VRN2-AS; and
VRN2-AI and VRN2-AJ.

79. A recombinant vector which comprises a nucleotide sequence selected from the group consisting of SEQ ID NO: 1, SEQ ID: NO: 3, SEQ ID NO: 4, SEQ ID NO: 6, and SEQ ID NO: 7 or a sequence degeneratively equivalent thereto.

80. A vector according to claim 79 wherein the nucleic acid comprised in the vector is capable of regulating one or more genes involved in the transition from vegetative to reproductive growth and/or capable of regulating one or more genes involved in the determination of leaf size and/or shape.

89. A plant according to claim 88 which is an agricultural or horticultural plant.

90. A plant according to claim 89 selected from the list consisting of: rice, maize, wheat, barley, oats, rye, oil seed rape, sugar beet, sunflower, soybean, sorghum, lettuce, endive, cabbage, broccoli, cauliflower, carnation, geranium, tobacco, cotton, canola, tomato, mango, peach, apple, pear, strawberry, banana, melon, carrot, onion, pea, celery.

91. A plant according to claim 90 which is selected from tobacco, oil seed rape, rice and wheat.

92. A part or propagule from a plant which is a clone, or selfed or hybrid progeny or other descendant of said transgenic plant, which in each case includes the plant cell transformed with a heterologous nucleic acid selected from the group consisting of SEQ ID NO: 1, SEQ ID: NO: 3, SEQ ID NO: 4, SEQ ID NO: 6, and SEQ ID NO: 7 and sequences degeneratively equivalent thereto.

93. An isolated polypeptide which is encoded by a nucleotide sequence according to claim 1.

94. A polypeptide according to claim 93 which comprises an amino acid sequence which consists of the sequence of SEQ ID Nos. 2, 5 or 8.

95. A polypeptide which is a fragment of a polypeptide of claim 94, having at least nine contiguous amino acids.

96. An isolated polypeptide which consists of the sequence of SEQ ID Nos. 2, 5 or 8.

97. An isolated polypeptide which is a fragment of a polypeptide according to claim 96 and which comprises at least 9 contiguous amino acids of that polypeptide.

which is capable of affecting one or more physical characteristics of a plant into which the nucleic acid is introduced, the physical characteristics being selected from vernalization response, flowering time, leaf size and/or shape or shade avoidance response or has promoter and/or regulatory function.

106. A method according to claim 105 which method comprises causing or allowing transcription from said nucleic acid thereby reducing VRN2 expression by co-suppression.

REMARKS

The purpose of this preliminary amendment is insert an abstract of the disclosure into the specification and to reinstate claims canceled in the first preliminary amendment.

Favorable consideration leading to prompt allowance of the present application is respectfully requested.

Respectfully submitted,
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